

DNA: AGTAGTGTACTACCAAGTATAGATAACGTTTGAATATTAAGTTTTGAATC 51  
 DNA: AAAGCCAAAGATGATTTGTATATTGGTGCTAATTACAGTTGCAGCTGCAAG 102  
 M(1): M I C I L V L I T V A A A S  
  
 DNA: CCCAGTGTATCAAAGGTGTTTCCAAGATGGGGCTATAGTGAAGCAAAACCC 153  
 M(15): P V Y Q R C F Q D G A I V K Q N P  
  
 DNA: ATCCAAAGAAGCAGTTACAGAGGTGTGCCTGAAAGATGATGTTAGCATGAT 204  
 M(32): S K E A V T E V C L K D D V S M I  
  
 DNA: CAAAACAGAGGCCAGGTATGTAAGAAATGCAACAGGAGTTTTTTTCAAATAA 255  
 M(49): K T E A R Y V R N A T G V F S N N  
  
 DNA: TGTGCAATAAGGAAATGGCTAGTCTCTGATTGGCATGATTGCAGGCCTAA 306  
 M(66): V A I R K W L V S D W H D C R P K  
  
 DNA: GAAGATCGTTGGGGGACACATCAATGTAATAGAAGTTGGTGATGACCTGTC 357  
 M(83): K I V G G H I N V I E V G D D L S  
  
 DNA: ACTCCATACTGAATCATATGTTTGCAGCGCAGATTGTACCATAGGTGTAGA 408  
 M(100): L H T E S Y V C S A D C T I G V D  
  
 DNA: CAAAGAGACTGCACAGGTTCAGGCTTCAGACAGATACCACAAATCATTTTGA 459  
 M(117): K E T A Q V R L Q T D T T N H F E  
  
 DNA: AATTGCAGGCACTACTGTGAAGTCAGGATGGTTCAAGAGCACGACATATAT 510  
 M(134): I A G T T V K S G W F K S T T Y I  
  
 DNA: AACTCTTGATCAAACCTTGCGAACACCTTAAAGTTTCC TGCGGCCCAAAATC 561  
 M(151): T L D Q T C E H L K V S C G P K S  
  
 DNA: TGTACAGTTCCATGCCTGCTTCAATCAGCATATGTCTTGCGTCAGATTTTT 612  
 M(168): V Q F H A C F N Q H M S C V R F L  
  
 DNA: ACACAGGACAATATTGCCTGGCTCTATAGCCAATTCCATATGTCAGAATAT 663  
 M(185): H R T I L P G S I A N S I C Q N I  
  
 DNA: CGAAATCATAATTTTAGTTACACTTACTCTATTAATCTTTATATTGTTAAG 714  
 M(202): E I I I L V T L T L L I F I L L S  
  
 DNA: CATTTTAAGTAAGACTTATATATGTTATTTATTAATGCCTATATTCATCCC 765  
 M(219): I L S K T Y I C Y L L M P I F I P  
  
 DNA: CATAGCATATATATACGGTATAATTTACAATAAGTCGTGCAAAAATGCAA 816  
 M(236): I A Y I Y G I I Y N K S C K K C K  
  
 DNA: ATTATGTGGCTTAGTGTATCATCCATTACAGAGTGTGGCACACATTGTGT 867  
 M(253): L C G L V Y H P F T E C G T H C V  
  
 DNA: CTGTGGTGCCCGCTATGATACTTCAGATAGAATGAACTGCATAGAGCTTC 918  
 M(270): C G A R Y D T S D R M K L H R A S  
  
 DNA: TGGATTGTGCCCTGGTTATAAAAGCCTAAGAGCTGCCAGAGTCATGTGCAA 969  
 M(287): G L C P G Y K S L R A A R//V M C K

FIG. 1A

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DNA: GTCGAAAGGGCCTGCATCAATATTGTCTATAATTACTGCGGTACTGGTCTT 1020  
M(304): S K G P A S I L S I I T A V L V L

DNA: AACCTTTGTGACACCAATCAACTCCATGGTTTTAGGAGAGAGTAAAGAAAC 1071  
M(321): T F V T P I N S M V L G E S K E T

DNA: CTTTGAACCTGAAGATCTTCCAGACGACATGTTGGAAATGGCATCGAGAAT 1122  
M(338): F E L E D L P D D M L E M A S R I

DNA: AAATTCTTATTATCTCACCTGTATCTTGAATTATGCTGTAAGCTGGGGTCT 1173  
M(355): N S Y Y L T C I L N Y A V S W G L

DNA: TGTTATCATTGGATTGTTGATCGGGCTGCTTTTTAAGAAATACCAGCACAG 1224  
M(372): V I I G L L I G L L F K K Y Q H R

DNA: ATTCTTAAATGTTTACGCAATGTACTGTGAAGAATGTGACATGTATCATGA 1275  
M(389): F L N V Y A M Y C E E C D M Y H D

DNA: CAAGTCTGGGTTGAAAAGACATGGTGATTTTACCAACAAATGCAGACAGTG 1326  
M(406): K S G L K R H G D F T N K C R Q C

DNA: CACATGTGGTCAATATGAAGATGCTGCAGGTTTGATGGCTCACAGGAAAAC 1377  
M(423): T C G Q Y E D A A G L M A H R K T

DNA: CTATAACTGCTTAGTGCAGTACAAAGCAAAGTGGATGATGAACTTCCTGAT 1428  
M(440): Y N C L V Q Y K A K W M M N F L I

DNA: AATTTACATATTCTTAATTTTGATCAAAGATTCTGCTATAGTTGTACAAGC 1479  
M(457): I Y I F L I L I K D S A I V V Q A/

DNA: TGCTGGAACCTGACTTCACCACCTGCCTAGAGACTGAGAGTATAAATTGGAA 1530  
M(474): /A G T D F T T C L E T E S I N W N

DNA: CTGCACTGGGCCATTTTTGAACCTCGGGAATTGCCAAAAGCAACAAAAGAA 1581  
M(491): C T G P F L N L G N C Q K Q Q K K

DNA: AGAACCTTACACCAACATTGCAACTCAGTTAAAGGGACTAAAGGCAATTTT 1632  
M(508): E P Y T N I A T Q L K G L K A I S

DNA: CGTACTAGATGTCCCTATAATAACAGGGATACCAGATGATATTGCGGGTGC 1683  
M(525): V L D V P I I T G I P D D I A G A

DNA: TTTAAGATATATAGAAGAGAAGGAAGATTTCCATGTCCAGCTAACTATAGA 1734  
M(542): L R Y I E E K E D F H V Q L T I E

DNA: ATATGCGATGTTAAGCAAATACTGTGACTATTATACCCAATTCTCAGATAA 1785  
M(559): Y A M L S K Y C D Y Y T Q F S D N

DNA: CTCAGGATACAGTCAGACAACATGGAGAGTGTACTTAAGGTCTCATGATTT 1836  
M(576): S G Y S Q T T W R V Y L R S H D F

DNA: TGAAGCCTGTATACTATATCCAAATCAGCACTTTTGCAGATGTGTAAAAAA 1887  
M(593): E A C I L Y P N Q H F C R C V K N

FIG. 1B

DNA: TGGTGAGAAAGTGCAGCAGCTCCAATTGGGACTTTGCCAATGAAATGAAAGA 1938  
M(610): G E K C S S S N W D F A N E M K D

DNA: TTATTACTCTGGGAAACAAACAAAGTTTGACAAGGACTTAAA TCTAGCCCT 1989  
M(627): Y Y S G K Q T K F D K D L N L A L

DNA: AACAGCTTTGCATCATGCCTTCAGGGGGACCTCATCTGCATA TATAGCAAC 2040  
M(644): T A L H H A F R G T S S A Y I A T

DNA: AATGCTCTCAAAAAAGTCCAATGATGACTTGATTGCATACACAAATAAGAT 2091  
M(661): M L S K K S N D D L I A Y T N K I

DNA: AAAAACAAAATTCCCAGGTAATGCATTGTTGAAGGCTATAATAGATTATAT 2142  
M(678): K T K F P G N A L L K A I I D Y I

DNA: AGCATATATGAAAAGTTTGCCAGGTATGGCAAATTTCAAATATGATGAATT 2193  
M(695): A Y M K S L P G M A N F K Y D E F

DNA: CTGGGATGAATTACTGTACAAACCCAAACCCAGCAAAGGCCTCAAACCTTGC 2244  
M(712): W D E L L Y K P N P A K A S N L A

DNA: TAGAGGAAAGGAGTCATCTTACAACCTCAAACCTAGCAATTTCAATCAAAGTC 2295  
M(729): R G K E S S Y N F K L A I S S K S

DNA: TATAAAAACCTGCAAGAATGTTAAGGATGTTGCCTGCTTATCGCCAAGGTC 2346  
M(746): I K T C K N V K D V A C L S P R S

DNA: AGGTGCTATATATGCTTCAATAATTGCGTGTGGTGAACCCAAT GGGCCAAG 2397  
M(763): G A I Y A S I I A C G E P N G P S

DNA: TGTGTATAGGAAACCATCAGGTGGTGTATTCCAATCTAGCACT GATCGGTC 2448  
M(780): V Y R K P S G G V F Q S S T D R S

DNA: TATATACTGCTTGCTGGATAGCCATTGTCTAGAAGAATTTGAG GCCATCGG 2499  
M(797): I Y C L L D S H C L E E F E A I G

DNA: CCAGGAGGAGCTGGATGCGGTAAAGAAATCCAAATGTTGGGAAATTGAATA 2550  
M(814): Q E E L D A V K K S K C W E I E Y

DNA: TCCTGACGTAAAGCTCATCCAAGAAGGCGATGGGACTAAAAGCTGTAGAAT 2601  
M(831): P D V K L I Q E G D G T K S C R M

DNA: GAAAGATTCTGGGAACTGCAATGTTGCAACTAACAGATGGCCAGTGATACA 2652  
M(848): K D S G N C N V A T N R W P V I Q

DNA: ATGTGAGAATGACAAATTTTACTACTCAGAGCTTCAAAAAGATTATGACAA 2703  
M(865): C E N D K F Y Y S E L Q K D Y D K

DNA: AGCTCAAGATATTGGTCACTATTGCTTAAGCCCTGGATGTACTACTGTCCG 2754  
M(882): A Q D I G H Y C L S P G C T T V R

DNA: GTACCCTATTAATCCAAAGCATCTCTAACTGTAATTGGCAAGTAAGCAG 2805  
M(899): Y P I N P K H I S N C N W Q V S R

FIG. 1C

DNA: ATCTAGCATAGCGAAGATAGATGTGCACAATATTGAGGATATTGAGCAATA 2856  
M(916): S S I A K I D V H N I E D I E Q Y

DNA: TAAGAAAGCTATAACTCAGAACTTCAAACGAGCCTATCTCTATTCAAGTA 2907  
M(933): K K A I T Q K L Q T S L S L F K Y

DNA: TGCAAAAACAAAAAAGCTTGCCGCACATCAAACCAATTTATAAATATATAAC 2958  
M(950): A K T K N L P H I K P I Y K Y I T

DNA: TATAGAAGGAACAGAACTGCAGAAGGTATAGAGAGTGCATACATTGAATC 3009  
M(967): I E G T E T A E G I E S A Y I E S

DNA: AGAAGTACCTGCATTGGCTGGGACATCTATCGGATTCAAAATCAATTCTAA 3060  
M(984): E V P A L A G T S I G F K I N S K

DNA: AGAGGGCAAGCACTTGCTAGATGTTATAGCATATGTAAAAAGTGCCTCATA 3111  
M(1001): E G K H L L D V I A Y V K S A S Y

DNA: CTCTTCAGTGTATACAAAATTGTACTCAACTGGCCCAACATCAGGGATAAA 3162  
M(1018): S S V Y T K L Y S T G P T S G I N

DNA: TACTAAACATGATGAATTGTGTACTGGCCCATGCCCAGCAAATATCAATCA 3213  
M(1035): T K H D E L C T G P C P A N I N H

DNA: TCAGGTTGGGTGGCTGACATTTGCAAGAGAGAGGACAAGCTCATGGGGATG 3264  
M(1052): Q V G W L T F A R E R T S S W G C

DNA: CGAAGAGTTTGGTTGCCTGGCTGTAAGTGATGGGTGTGTATTGGATCATG 3315  
M(1069): E E F G C L A V S D G C V F G S C

DNA: CCAAGATATAATAAAAGAAGAACTATCTGTCTATAGGAAGGAGACCGAGGA 3366  
M(1086): Q D I I K E E L S V Y R K E T E E

DNA: AGTGACTGATGTAGAACTGTGTTTGACATTTTCAGACAAAACATACTGTAC 3417  
M(1103): V T D V E L C L T F S D K T Y C T

DNA: AAAGTTAAACCCTGTTACCCCTATTATAACAGATCTATTTGAGGTACAGTT 3468  
M(1120): N L N P V T P I I T D L F E V Q F

DNA: CAAAAGTGTAGAGACCTACAGCTTGCCTAGAATTGTTGCTGTGCAAAACCA 3519  
M(1137): K T V E T Y S L P R I V A V Q N H

DNA: TGAGATTAAAATTGGGCAAATAAATGATTTAGGAGTTTACTCTAAGGGTTG 3570  
M(1154): E I K I G Q I N D L G V Y S K G C

DNA: TGGGAATGTTCAAAGGTCAATGGAAGTATTTATGGCAATGGAGTTCCCAG 3621  
M(1171): G N V Q K V N G T I Y G N G V P R

DNA: ATTTGACTACTTATGCCATTTAGCTAGCAGGAAGGAAGTCATTGTTAGAAA 3672  
M(1188): F D Y L C H L A S R K E V I V R K

DNA: ATGCTTCGACAATGATTACCAAGCATGCAAATTTCTTCAAAGCCCTGCTAG 3723  
M(1205): C F D N D Y Q A C K F L Q S P A S

FIG. 1D

DNA: TTACAGACTTGAAGAAGACAGTGGCACTGTGACCATAATTGACTACAAAAA	3774
M(1222): Y R L E E D S G T V T I I D Y K K	
DNA: GATTTTAGGAACAATCAAGATGAAGGCAATTTTAGGAGATGTCAAATATAA	3825
M(1239): I L G T I K M K A I L G D V K Y K	
DNA: AACATTTGCTGATAGTGTGCGATATAACCGCAGAAGGGTCATGCACCGGCTG	3876
M(1256): T F A D S V D I T A E G S C T G C	
DNA: TATTAAGTCTTCGAAAATATCCATTGCGAATTAACGTTGCACACCACAAT	3927
M(1273): I N C F E N I H C E L T L H T T I	
DNA: TGAAGCCAGCTGCCCAATTAAAAGCTCGTGCACAGTATTTTCATGACAGGAT	3978
M(1290): E A S C P I K S S C T V F H D R I	
DNA: TCTTGTGACTCCAAATGAACACAAATATGCATTGAAAATGGTGTGCACAGA	4029
M(1307): L V T P N E H K Y A L K M V C T E	
DNA: AAAGCCAGGGAACACACTCACAATTAAAGTCTGCAATACTAAAAGTTGAAGC	4080
M(1324): K P G N T L T I K V C N T K V E A	
DNA: ATCTATGGCCCTTG TAGACGCAAAGCCTATCATAGAACTAGCACCAGTTGA	4131
M(1341): S M A L V D A K P I I E L A P V D	
DNA: TCAGACAGCATATATAAGAGAAAAAGATGAAAGGTGTAAACTTGGATGTG	4182
M(1358): Q T A Y I R E K D E R C K T W M C	
DNA: TAGGGTAAGAGATGAAGGACTGCAGGTCATCTTGGAGCCATTTAAAAATTT	4233
M(1375): R V R D E G L Q V I L E P F K N L	
DNA: ATTTGGATCTTATATTGGGATATTTTACACATTTATTATATCTATAGTAGT	4284
M(1392): F G S Y I G I F Y T F I I S I V V	
DNA: ATTATTGGTTATTATCTATGTACTACTACCTATATGCTTTAAGTTAAGGGA	4335
M(1409): L L V I I Y V L L P I C F K L R D	
DNA: TACCCTTAGAAAGCATGAAGATGCATATAAGAGAGAGATGAAAATTAGATA	4386
M(1426): T L R K H E D A Y K R E M K I R ●	
DNA: GGGGATCTATGCAGAACAAAATTGAGTCCTGTATTATATACTTCTATTTGT	4437
DNA: AGTATAGCTGTTGTTAAGTGGGGGTGGGGAAC TAACAACAGCGTAAATTT	4488
DNA: ATTTTGCAACATTATTTTATACTTGGTAGCACACTACT	4527

FIG. 1E

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DNA: AGTAGTGTACCCCACTTGAATACTTTGAAAATAAATTGTTGTTGACTGTTT 51  
 DNA: TTTACCTAAGGGGAAATTATCAAGAGTGTGATGTCGGATTGGTGTTTTAT 1 02  
 N(1): M S D L V F Y  
 NSs(1): M

DNA: GATGTCGCATCAACAGGTGCAAATGGATTGATCCTGATGCAGGGTATATG 1 53  
 N(8): D V A S T G A N G F D P D A G Y M  
 NSs(2): M S H Q Q V Q M D L I L M Q G I W

DNA: GACTTCTGTGTTAAAAATGCAGAATTACTCAACCTTGCTGCAGTTAGGATC 2 04  
 N(25): D F C V K N A E L L N L A A V R I  
 NSs(19): T S V L K M Q N Y S T L L Q L G S

DNA: TTCTTCCTCAATGCCGCAAAGGCCAAGGCTGCTCTCTCGCGTAAGCCAGAG 2 55  
 N(42): F F L N A A K A K A A L S R K P E  
 NSs(36): S S S M P Q R P R L L S R V S Q R

DNA: AGGAAGGCTAACCCTAAATTTGGAGAGTGGCAGGTGGAGGTTATCAATAAT 3 06  
 N(59): R K A N P K F G E W Q V E V I N N  
 NSs(53): G R L T L N L E S G R W R L S I I

DNA: CATTTTCCTGGAAACAGGAACAACCCAATTGGTAACAACGATCTTACCATC 3 57  
 N(76): H F P G N R N N P I G N N D L T I  
 NSs(70): I F L E T G T T Q L V T T I L P S

DNA: CACAGATTATCTGGGTATTTAGCCAGATGGGTCCTTGATCAGTATAACGAG 4 08  
 N(93): H R L S G Y L A R W V L D Q Y N E  
 NSs(87): T D Y L G I

DNA: AATGATGATGAGTCTCAGCACGAGTTGATCAGAACAACCTATTATCAACCCA 4 59  
 N(110): N D D E S Q H E L I R T T I I N P

DNA: ATTGCTGAGTCTAATGGTGTAGGATGGGACAGTGGGCCAGAGATCTATCTA 5 10  
 N(127): I A E S N G V G W D S G P E I Y L

DNA: TCATTCTTTCCAGGAACAGAAATGTTTTTGGAACTTTCAAATTCTACCCG 5 61  
 N(144): S F F P G T E M F L E T F K F Y P

DNA: CTGACCATTGGAATTCACAGAGTCAAGCAAGGCATGATGGACCCTCAATAC 6 12  
 N(161): L T I G I H R V K Q G M M D P Q Y

DNA: CTGAAGAAGGCCTTAAGGCAACGCTATGGCACTCTCACAGCAGATAAGTGG 6 63  
 N(178): L K K A L R Q R Y G T L T A D K W

DNA: ATGTCACAGAAGGTTGCAGCAATTGCTAAGAGCCTGAAGGATGTAGAGCAG 7 14  
 N(195): M S Q K V A A I A K S L K D V E Q

FIG. 2A

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DNA: CTTAAATGGGGAAAAGGAGGCCTGAGCGATACTGCTAAAACATTCCTGCAG	765
N(212): L K W G K G G L S D T A K T F L Q	
DNA: AAATTGGCATCAGGCTTCCATAAATATGGCATGAGGCATTCAAATTAGGT	816
N(229): K F G I R L P ●	
DNA: TCTAAATTCTAAATTTATATATGTCAATTTGATTAATTGGTTATCCAAAAG	867
DNA: GGTTTTCTTAAGGGAACCCACAAAAATAGCAGCTAAATGGGTGGGTGGTAG	918
DNA: GGGACAGCAAAAACTATAAATCAGGTCATAAATAAAATAAAATGTATTCA	969
DNA: GTGGGGCACACTACT	984

FIG. 2B

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DNA: AGTAGTGTA	51
DNA: TATATGCATAATGGACTATCAAGAGTATCAACAATTCTTGGCTAGGATTAA	102
(L1): M D Y Q E Y Q Q F L A R I N	
DNA: TACTGCAAGGGATGCATGTGTAGCCAAGGATATCGATGTTGACCTATTAAT	153
(L15): T A R D A C V A K D I D V D L L M	
DNA: GGCCAGACATGATTATTTTGGTAGAGAGCTGTGCAAGTCCTTAAATATAGA	204
(L32): A R H D Y F G R E L C K S L N I E	
DNA: ATATAGGAATGATGTACCATTTGTAGATATAATTTTGGATATAAGGCCCGA	255
(L49): Y R N D V P F V D I I L D I R P E	
DNA: AGTAGACCCATTAACCATAGATGCACCACATATTACCCCAGACAATTATCT	306
(L66): V D P L T I D A P H I T P D N Y L	
DNA: ATATATAAATAATGTGTTATATATCATAGATTATAAGGTCTCTGTATCGAA	357
(L83): Y I N N V L Y I I D Y K V S V S N	
DNA: TGAAAGCAGTGTTATAACATATGACAAATATTATGAGTTAACTAGGGACAT	408
(L100): E S S V I T Y D K Y Y E L T R D I	
DNA: ATCCGATAGATTAAGTATTCCAATAGAAATAGTTATCGTCCGTATAGACCC	459
(L117): S D R L S I P I E I V I V R I D P	
DNA: TGTAAGTAAGGATTTGCATATTAACTCTGATAGATTTAAAGAACTTTACCC	510
(L134): V S K D L H I N S D R F K E L Y P	
DNA: TACAATAGTGGTGGATATAAACTTCAATCAATTTTTCGACTTAAACAATT	561
(L151): T I V V D I N F N Q F F D L K Q L	
DNA: ACTCTATGAAAAATTCGGTGATGATGAAGAATTCCTATTGAAAGTTGCACA	612
(L168): L Y E K F G D D E E F L L K V A H	
DNA: TGGTGACTTCACTCTTACAGCACCCCTGGTGCAAGACTGGGTGCCCTGAATT	663
(L185): G D F T L T A P W C K T G C P E F	
DNA: TTGGAAACACCCCATTTATAAAGAATTTAAATGAGTATGCCAGTACCTGA	714
(L202): W K H P I Y K E F K M S M P V P E	
DNA: GCGGAGGCTCTTTGAAGAATCTGTCAAGTTCAATGCTTATGAATCTGAGAG	765
(L219): R R L F E E S V K F N A Y E S E R	
DNA: ATGGAATACTAACTTGGTTAAAAATCAGAGAATATACAAAGAAAGACTATTC	816
(L236): W N T N L V K I R E Y T K K D Y S	
DNA: AGAGCATATTTCAAATCTGCAAAAAATATTTTCCTGGCTAGTGGATTTTA	867
(L253): E H I S K S A K N I F L A S G F Y	
DNA: TAAGCAGCCAAATAAGAATGAGATTAGTGAGGGGTGGACATTAATGGTTGA	918
(L270): K Q P N K N E I S E G W T L M V E	
DNA: GAGGGTTCAAGATCAGAGAGAAATCTCAAATCTCTCCATGACCAGAAACC	969
(L287): R V Q D Q R E I S K S L H D Q K P	

FIG. 3A



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DNA: TAGCATACATTTTATATGGGGAGCCCATAACCCAGGAAATAGTAATAATGC (L304): S I H F I W G A H N P G N S N N A	1020
DNA: AACCTTCAAACCTCATATTGCTTTCAAAGTCCTTACAAAGCATAAAAGGTAT (L321): T F K L I L L S K S L Q S I K G I	1071
DNA: ATCAACTTACACAGAAGCGTTCAAATCTTTAGGAAAAATGATGGATATTGG (L338): S T Y T E A F K S L G K M M D I G	1122
DNA: AGATAAGGCTATTGAGTATGAAGAATTCTGCATGTCCCTAAAAAGCAAAGC (L355): D K A I E Y E E F C M S L K S K A	1173
DNA: AAGATCATCATGGAAGCAAATAATGAACAAAAAATTAGAGCCTAAACAAAT (L372): R S S W K Q I M N K K L E P K Q I	1224
DNA: AAACAATGCCCTTGTTTTATGGGAACAGCAGTTTATGGTAAATAATGACCT (L389): N N A L V L W E Q Q F M V N N D L	1275
DNA: GATAGACAAAAGTGAGAAGTTGAAATTATTCAAAAATTTCTGCGGTATAGG (L406): I D K S E K L K L F K N F C G I G	1326
DNA: CAAACACAAGCAATTCAAGAATAAAATGCTAGAGGATCTAGAAGTGTCAAA (L423): K H K Q F K N K M L E D L E V S K	1377
DNA: GCCCAAAATATTAGACTTTGATGACGCAAATATGTATCTAGCTAGCCTAAC (L440): P K I L D F D D A N M Y L A S L T	1428
DNA: CATGATGGAACAGAGTAAGAAGATATTGTCCAAAAGCAATGGGTGAAGCC (L457): M M E Q S K K I L S K S N G L K P	1479
DNA: AGATAATTTTATACTGAATGAATTTGGATCCAAAATCAAAGATGCTAATAA (L474): D N F I L N E F G S K I K D A N K	1530
DNA: AGAAACATATGACAATATGCACAAAATATTGAGACAAGATATTGGCAATG (L491): E T Y D N M H K I F E T R Y W Q C	1581
DNA: TATATCCGACTTCTCTACTCTGATGAAAAATATCTTATCTGTGTCCCAATA (L508): I S D F S T L M K N I L S V S Q Y	1632
DNA: TAACAGGCACAACACATTTAGGATAGCTATGTGTGCTAATAACAATGTCTT (L525): N R H N T F R I A M C A N N N V F	1683
DNA: TGCTATAGTATTTTCTTCGGCTGACATAAAAACTAAGAAAGCAACTGTAGT (L542): A I V F P S A D I K T K K A T V V	1734
DNA: TTATAGCATTATAGTGCTGCATAAAGAGGAAGAAAACATATTCAACCCAGG (L559): Y S I I V L H K E E E N I F N P G	1785
DNA: ATGTTTGCACGGCACATTTAAGTGTATGAATGGGTATATTTCCATATCTAG (L576): C L H G T F K C M N G Y I S I S R	1836
DNA: AGCTATAAGGCTAGATAAAGAGAGGTGCCAGAGAATTGTTTCCTCACCTGG (L593): A I R L D K E R C Q R I V S S P G	1887

FIG. 3B

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DNA: ACTGTTTTTAACAACCTTGCCTACTATTCAAACATGATAATCCAACCTCTAGT 1938  
(L610): L F L T T C L L F K H D N P T L V

DNA: GATGAGCGATATTATGAATTTTTCTATATACACTAGCCTGTCTATCACAAA 1989  
(L627): M S D I M N F S I Y T S L S I T K

DNA: GAGTGTTCCTATCTTTAACAGAGCCAGCAGCTACATGATTATGAACCTCATT 2040  
(L644): S V L S L T E P A R Y M I M N S L

DNA: AGCTATCTCCAGCAATGTTAAGGACTATATAGCAGAGAAATTTTCCCCTTA 2091  
(L661): A I S S N V K D Y I A E K F S P Y

DNA: CACAAAGACACTGTTCACTGTCTATATGACTAGACTAATTAAAAATGCTTG 2142  
(L678): T K T L F S V Y M T R L I K N A C

DNA: CTTTGATGCTTATGACCAGAGACAGCGTGTCCAACCTTAGAGATATATATTT 2193  
(L695): F D A Y D Q R Q R V Q L R D I Y L

DNA: ATCTGATTATGACATAACCCAAAAGGTATTAAAGACAATAGAGAGCTAAC 2244  
(L712): S D Y D I T Q K G I K D N R E L T

DNA: AAGTATATGGTTCCTGGTAGTGTAAACATTAAAGGAGTATTTAACACAAAT 2295  
(L729): S I W F P G S V T L K E Y L T Q I

DNA: ATACTTACCATTTTATTTTAAATGCTAAAGGACTACATGAGAAGCACCATGT 2346  
(L746): Y L P F Y F N A K G L H E K H H V

DNA: CATGGTGGATCTAGCAAAGACTATATTAGAAATAGAGTGCGAACAGAGGGA 2397  
(L763): M V D L A K T I L E I E C E Q R E

DNA: AAACATAAAGGAGATATGGTCTACAAATTGTACCAAACAGACAGTGAACCT 2448  
(L780): N I K E I W S T N C T K Q T V N L

DNA: TAAATTTTGTATCCATTCCTTGTGCAAGAATTTACTAGCAGACACTTCAAG 2499  
(L797): K I L I H S L C K N L L A D T S R

DNA: ACACAACCACTTGCGGAACAGAATAGAAAATAGGAACAATTTTAGAAGGTC 2550  
(L814): H N H L R N R I E N R N N F R R S

DNA: TATAACAACCTATTTCAACATTTACAAGTTCAAAGTCTTGCCTCAAAATAGG 2601  
(L831): I T T I S T F T S S K S C L K I G

DNA: GGACTTTAGAAAAGAGAAAAGAGCTGCAGTCAGTTAAACAGAAGAAAATCTT 2652  
(L848): D F R K E K E L Q S V K Q K K I L

DNA: AGAGGTGCAGAGTCGCAAAATGAGATTAGCAAACCCAATGTTTCGTGACAGA 2703  
(L865): E V Q S R K M R L A N P M F V T D

DNA: TGAACAAGTATGCCTTGAAGTTGGGCACTGCAATTATGAGATGCTGAGGAA 2754  
(L882): E Q V C L E V G H C N Y E M L R N

DNA: TGCTATGCCGAATTATACAGATTATATATCAACTAAAGTATTTGATAGGTT 2805  
(L899): A M P N Y T D Y I S T K V F D R L

FIG. 3C

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DNA: ATATGAGTTATTAGATAAAGGAGTTTTGACAGACAAGCCTGTTATAGAGCA (L916): Y E L L D K G V L T D K P V I E Q	2856
DNA: AATAATGGATATGATGGTCGACCACAAAAAGTTCTATTTCACATTTTTCAA (L933): I M D M M V D H K K F Y F T F F N	2907
DNA: TAAAGGCCAGAAAACGTCAAAGGATAGAGAGATATTCGTTGGAGAATATGA (L950): K G Q K T S K D R E I F V G E Y E	2958
DNA: AGCTAAAATGTGTATGTACGCAGTTGAGAGAATAGCAAAAAGAAAGATGTAA (L967): A K M C M Y A V E R I A K E R C K	3009
DNA: ATTAAATCCTGATGAAATGATATCTGAGCCGGGTGATGGCAAGTTGAAGGT (L984): L N P D E M I S E P G D G K L K V	3060
DNA: GTTGGAGCAAAAATCAGAACAAGAAATTCGATTCTTGGTCGAGACTACAAG (L1001): L E Q K S E Q E I R F L V E T T R	3111
DNA: GCAAAAGAATCGTGAAATCGATGAGGCAATTGAAGCATTAGCTGCAGAAGG (L1018): Q K N R E I D E A I E A L A A E G	3162
DNA: ATATGAGAGTAATCTAGAAAAAATTGAAAAGCTTTCACCTGGCAAAGCAAA (L1035): Y E S N L E K I E K L S L G K A K	3213
DNA: GGGCCTAAAGATGGAAATAAATGCAGATATGTCTAAATGGAGTGCTCAGGA (L1052): G L K M E I N A D M S K W S A Q D	3264
DNA: TGTTTTTTATAAATATTTCTGGCTCATAGCCTTAGACCCTATCCTCTACCC (L1069): V F Y K Y F W L I A L D P I L Y P	3315
DNA: ACAGGAAAAAGAGAGAATATTATACTTTATGTGCAACTACATGGATAAAGA (L1086): Q E K E R I L Y F M C N Y M D K E	3366
DNA: ATTGATACTGCCAGATGAATTATTATTCAATTTGCTGGACCAAAAAGTTGC (L1103): L I L P D E L L F N L L D Q K V A	3417
DNA: ATACCAGAATGATATAATAGCTACTATGACTAATCAATTAAATTCAAATAC (L1120): Y Q N D I I A T M T N Q L N S N T	3468
DNA: AGTTCTGATAAAGAGAAATTGGCTCCAAGGGAATTTCAACTACACCTCAAG (L1137): V L I K R N W L Q G N F N Y T S S	3519
DNA: TTACGTCCATAGCTGCGCAATGTCTGTGTATAAAGAAATATTAAAAAGAGGC (L1154): Y V H S C A M S V Y K E I L K E A	3570
DNA: CATAACATTACTAGACGGGTCTATATTAGTCAACTCATTAGTCCATTTCGGA (L1171): I T L L D G S I L V N S L V H S D	3621
DNA: TGATAACCAAACATCGATAACAATAGTTCAGGATAAGATGGAAAATGATAA (L1188): D N Q T S I T I V Q D K M E N D K	3672
DNA: AATTATAGATTTTGCAATGAAAGAATTTGAGAGAGCCTGTTTGACATTTGG (L1205): I I D F A M K E F E R A C L T F G	3723

FIG. 3D

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DNA: ATGCCAAGCAAATATGAAAAAGACATATGTAACAAATTGCATAAAAGAGTT 3774  
(L1222): C Q A N M K K T Y V T N C I K E F

DNA: TGTTTCATTATTTAACTTGTACGGCGAACCCTTTTCAATATATGGCAGATT 3825  
(L1239): V S L F N L Y G E P F S I Y G R F

DNA: CCTATTAACATCTGTGGGTGATTGTGCCTATATAGGGCCTTATGAAGATTT 3876  
(L1256): L L T S V G D C A Y I G P Y E D L

DNA: AGCTAGTCGAATATCATCAGCCCAGACAGCCATAAAGCATGGTTGTCCACC 3927  
(L1273): A S R I S S A Q T A I K H G C P P

DNA: CAGTCTAGCATGGGTGTCCATAGCAATAAGTCATTGGATGACCTCTCTGAC 3978  
(L1290): S L A W V S I A I S H W M T S L T

DNA: ATACAACATGCTACCAGGGCAGTCAAATGACCCAATTGATTATTTCCCTGC 4029  
(L1307): Y N M L P G Q S N D P I D Y F P A

DNA: AGAAAAATAGGAAGGATATCCCTATAGAATTGAATGGTGTATTAGATGCTCC 4080  
(L1324): E N R K D I P I E L N G V L D A P

DNA: ATTGTCAATGATTAGTACAGTTGGATTGGAATCTGGGAATTTATACTTCTT 4131  
(L1341): L S M I S T V G L E S G N L Y F L

DNA: GATAAAGTTGTTGAGCAAATATACCCCGGTCATGCAGAAAAGAGAGTCAGT 4182  
(L1358): I K L L S K Y T P V M Q K R E S V

DNA: AGTCAACCAAATAGCTGAAGTTAAGAACTGGAAGGTCGAGGATCTAACAGA 4233  
(L1375): V N Q I A E V K N W K V E D L T D

DNA: CAATGAAATATTTAGACTTAAAATACTCAGATATTTAGTTCTAGATGCAGA 4284  
(L1392): N E I F R L K I L R Y L V L D A E

DNA: GATGGACCCTAGTGATATTATGGGTGAGACAAGCGACATGAGAGGGAGGTC 4335  
(L1409): M D P S D I M G E T S D M R G R S

DNA: TATTTTGACACCTAGAAAATTCACAACAGCAGGCAGTTTAAGGAAATTATA 4386  
(L1426): I L T P R K F T T A G S L R K L Y

DNA: TTCTTTCAGTAAGTACCAGGATAGACTGTCTTCCCCTGGAGGCATGGTTGA 4437  
(L1443): S F S K Y Q D R L S S P G G M V E

DNA: ATTGTTCACTTATTTGCTTGAGAAAACCTGAGTTGTTAGTGAATAAGGGGA 4488  
(L1460): L F T Y L L E K P E L L V T K G E

DNA: AGATATGAAAGATTATATGGAATCTGTGATATTCCGATATAATTCCAAAAG 4539  
(L1477): D M K D Y M E S V I F R Y N S K R

DNA: GTTCAAAGAAAGTTTGTCAATACAGAACCCAGCACAAATTATTTATAGAACA 4590  
(L1494): F K E S L S I Q N P A Q L F I E Q

DNA: GATATTGTTCTCACATAAGCCCATAATAGACTTTTCTGGTATCAGGGACAA 4641  
(L1511): I L F S H K P I I D F S G I R D K

FIG. 3E

DNA: ATATATAAACCTACATGATAGTAGAGCTCTAGAGAAGGAACCTGACATATT 4692  
(L1528): Y I N L H D S R A L E K E P D I L

DNA: AGGAAAAGTAACATTTACAGAGGCTTATAGATTATTAATGAGGGACCTGTC 4743  
(L1545): G K V T F T E A Y R L L M R D L S

DNA: TAGCCTAGAACTAACCAATGATGACATTCAAGTAATTTATTCTTACATAAT 4794  
(L1562): S L E L T N D D I Q V I Y S Y I I

DNA: ACTTAATGACCCTATGATGATAACTATTGCAAACACACATATATTGTCAAT 4845  
(L1579): L N D P M M I T I A N T H I L S I

DNA: ATACGGGAGTCCTCAACGGAGGATGGGCATGTCCTGTTCAACGATGCCAGA 4896  
(L1596): Y G S P Q R R M G M S C S T M P E

DNA: ATTTAGAAAATTTAAAATTAATACATCATTCCCCAGCCTTAGTTTTGAGAGC 4947  
(L1613): F R N L K L I H H S P A L V L R A

DNA: ATATAGTAAAAATAATCCTGACATCCAGGGTGCTGATCCACGGAAATGGC 4998  
(L1630): Y S K N N P D I Q G A D P T E M A

DNA: TAGAGATTTAGTTCATCTGAAAGAGTTTGTTGAGAACACAAATTTAGAAGA 5049  
(L1647): R D L V H L K E F V E N T N L E E

DNA: AAAAATGAAAGTTAGGATTGCTATAAATGAAGCAGAGAAAGGACAACGGGA 5100  
(L1664): K M K V R I A I N E A E K G Q R D

DNA: TATAGTCTTTGAACTAAAAGAGATGACTAGATTTTATCAGGTTTGCTATGA 5151  
(L1681): I V F E L K E M T R F Y Q V C Y E

DNA: GTATGTCAAATCTACAGAACACAAGATAAAAGTCTTCATTCTCCCGACAAA 5202  
(L1698): Y V K S T E H K I K V F I L P T K

DNA: ATCATACACAACAACAGATTTCTGTTCATCATGCAGGGGAATTTAATAAA 5253  
(L1715): S Y T T T D F C S L M Q G N L I K

DNA: AGATAAAGAGTGGTACACAGTTCACTACCTAAAACAGATATTGTCTGGTGG 5304  
(L1732): D K E W Y T V H Y L K Q I L S G G

DNA: CCATAAAGCCATAATGCAGCATAATGCCACTAGTGAGCAAAATATTGCTTT 5355  
(L1749): H K A I M Q H N A T S E Q N I A F

DNA: TGAGTGTTTCAAATTAATTACCCATTTTGCAGACTCATTATAGATTTCATT 5406  
(L1766): E C F K L I T H F A D S F I D S L

DNA: ATCTAGGTCAGCTTTTTTGCAGTTGATAATAGATGAATTCAGTTATAAAGA 5457  
(L1783): S R S A F L Q L I I D E F S Y K D

DNA: TGTGAAGGTTAGCAAACTTTATGACATAATAAAGAATGGGTATAATCGAAC 5508  
(L1800): V K V S K L Y D I I K N G Y N R T

DNA: TGACTTCATACCATTTGCTTTTTAGAACTGGCGATTTAAGACAAGCTGACTT 5559  
(L1817): D F I P L L F R T G D L R Q A D L

FIG. 3F

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DNA: AGACAAGTATGATGCTATGAAAAGTCATGAGAGGGTTACATGGAATGATTG 5610  
 (L1834): D K Y D A M K S H E R V T W N D W

DNA: GCAAACATCTCGTCACTTGGACATGGGCTCAATTAATCTAACAATAACCGG 5661  
 (L1851): Q T S R H L D M G S I N L T I T G

DNA: TTACAATAGATCAATAACAATAATCGGAGAAGATAACAAATTGACATATGC 5712  
 (L1868): Y N R S I T I I G E D N K L T Y A

DNA: AGAATTATGTCTGACTAGGAAAACCTCTGAGAATATAACTATAAGTGGCAG 5763  
 (L1885): E L C L T R K T P E N I T I S G R

DNA: AAAATTGCTAGGTGCAAGGCATGGACTTAAATTTGAAAATATGTCCAAAAT 5814  
 (L1902): K L L G A R H G L K F E N M S K I

DNA: CCAAACATACCCAGGCAATTATTATATAACATATAGAAAGAAAGATCGCCA 5865  
 (L1919): Q T Y P G N Y Y I T Y R K K D R H

DNA: CCAGTTTGTATACCAGATACATTCTCATGAATCAATAACAAGGAGGAATGA 5916  
 (L1936): Q F V Y Q I H S H E S I T R R N E

DNA: AGAGCATATGGCTATCAGGACCAGAATATACAATGAAATAACTCCAGTATG 5967  
 (L1953): E H M A I R T R I Y N E I T P V C

DNA: TGTAGTTAACGTTGCAGAGGTGGATGGGGACCAACGTATATTGATAAGATC 6018  
 (L1970): V V N V A E V D G D Q R I L I R S

DNA: TTTAGACTATCTAAATAATGATATATTTTCTCTTTCAAGGATTAAAGTCGG 6069  
 (L1987): L D Y L N N D I F S L S R I K V G

DNA: GCTTGACGAATTTGCAACAATAAAAAAAGCACACTTTAGTAAATGGTCTC 6120  
 (L2004): L D E F A T I K K A H F S K M V S

DNA: ATTTGAAGGACCCCCAATTAAGACAGGGCTCCTCGACCTTACTGAATTGAT 6171  
 (L2021): F E G P P I K T G L L D L T E L M

DNA: GAAATCTCAAGATTTGCTTAACCTTAATTATGATAATATAAGGAATAGCAA 6222  
 (L2038): K S Q D L L N L N Y D N I R N S N

DNA: CTTGATATCTTTTTCAAATGATTGCTGTGAGGGGTCAGATAATATAAA 6273  
 (L2055): L I S F S K L I C C E G S D N I N

DNA: TGATGGGTAGAGTTTCTGTCCGATGACCCTATGAACCTTTACAGAGGGTGA 6324  
 (L2072): D G L E F L S D D P M N F T E G E

DNA: AGCAATACATTCAACACCGATCTTTAATATATATTACTCAAAAAGAGGAGA 6375  
 (L2089): A I H S T P I F N I Y Y S K R G E

DNA: AAGACATATGACATACAGGAATGCAATTAAATTACTGATAGAAAGAGAAAC 6426  
 (L2106): R H M T Y R N A I K L L I E R E T

DNA: TAAGATTTTGAAGAAGCTTTCACATTCAAGTGAGAATGGCTTCATATCGCC 6477  
 (L2123): K I F E E A F T F S E N G F I S P

FIG. 3G

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## FIG. 3H

DNA: AGAATCTTGGTTGCTTGAAGCAGTATCATTAATAAATTGTTGAA (L2140): E N L G C L E A V V S L I K L K  
DNA: AACTAATGAGTGGTCCACAGTTATAGATTAATGTTATGTTAAT (L2157): T N E W S T V I D K C I H I C L I  
DNA: AAAGAATGGTATGGATCCACATGTTACCATTCATTTGATGTCCTTAATAATGTTT (L2174): K N G M D H M Y H S F D V P K C F  
DNA: TATGGGAATCCTATCAGACATGTAATGGATGATGTTTATGAGAAATT (L2191): M G N P I T R D M N W M M F R E F  
DNA: CATCAATAGTTTACCGAGGACAGATATACCAATGGAATGTCATGACAGA (L2208): I N S L P G T D I P W N V M T E  
DNA: GAACCTCAAAAAGAAAATGTAATTGCTCTGATTAACCTCTAAGTTAGAAAACACA (L2225): N F K K K C I A L I N S K L E T Q  
DNA: GAGAGATTTCTCAGAAATTCACCTAAACTGATGAAGGAAGGAGGAGGAG (L2242): R D F S E F T K L M K K E G G R S  
DNA: TAATATAGAAATTTGATTTAGTTATGAGTTTACAGAGAACCTTACAAATTAG (L2259): N I E F D ●  
DNA: GCTATAAATTTGGGAGGGTTTGGAAAATTTGGCTTAAAAATTCAAAAAGAGGGG  
DNA: GATTAAACAGCAACTGTATTAATTTTGATAGATGAGGGGCCACACTACT



A primer = cDNA primer = sense primer = forward primer =

**B primer = antisense primer=reverse primer =**

V = viral genome, minus (-) strand = \_\_\_\_\_

cV = viral antigenomic, plus strand (+) = —

cDNA or cRNA = complementary DNA or RNA= - - - - -

**FIG. 4A**



P1 = probe (sense or antisense) or capture oligo (sense or antisense)

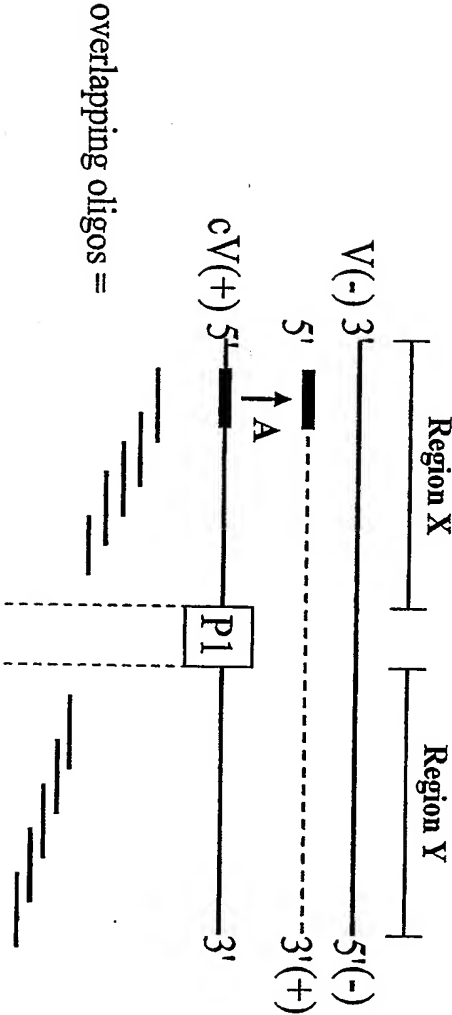


FIG. 4B

P1 = sense, cDNA primer (A)

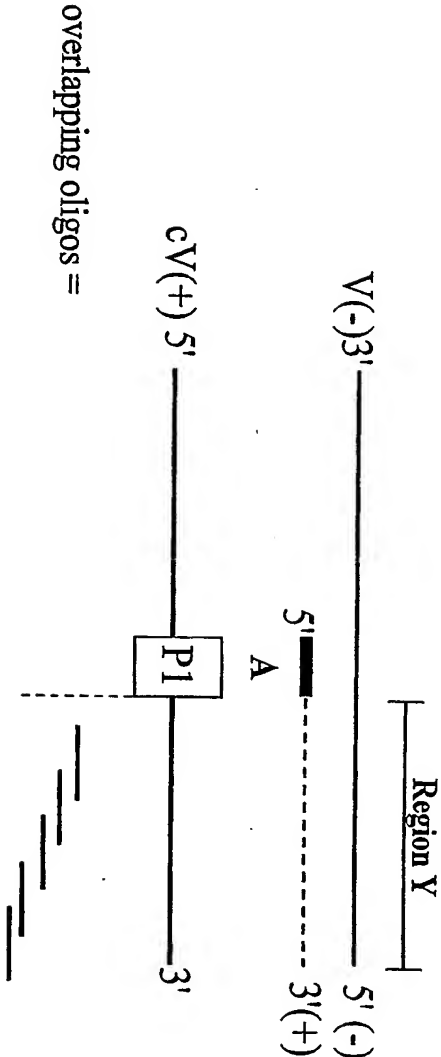


FIG. 4C

P1 = reverse, antisense primer (B)

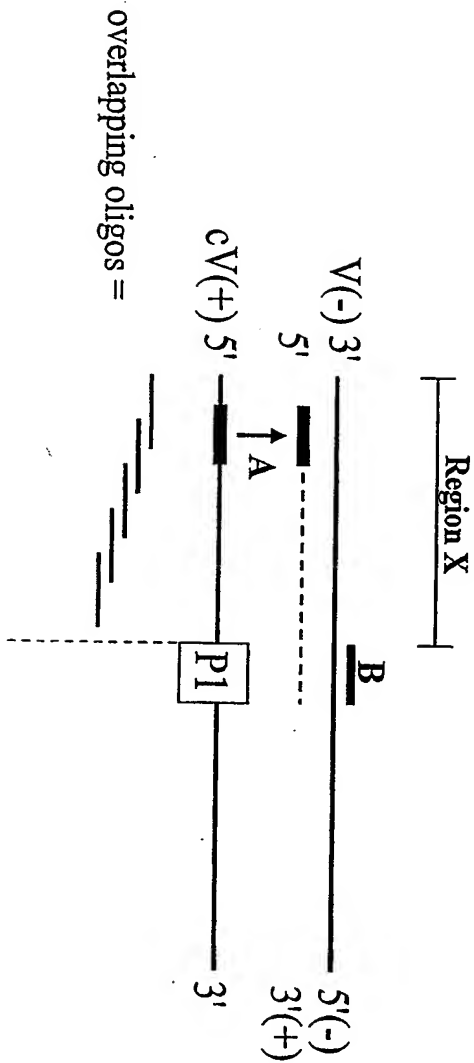


FIG. 4D

P1 = sense, cDNA primer and P2 = reverse, antisense primer

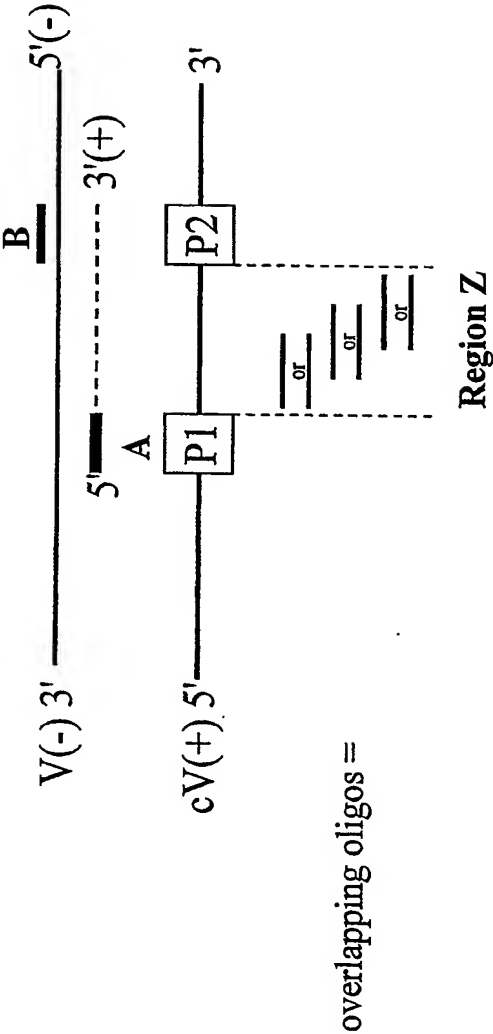


FIG. 4E

P1 = sense, cDNA primer and P2 = probe (sense or antisense)

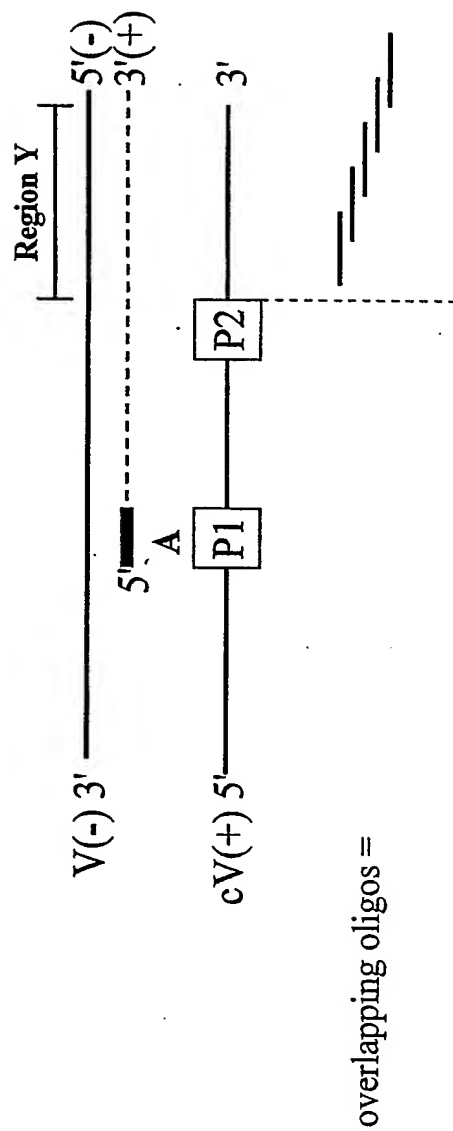


FIG. 4F

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FIG. 5A

## Forward Primer

Start	Length	Tm	%GC	Primer
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
1470	25	60	44	TTGTACAAGCTGCTGGAAGTGAAGT
869	22	60	50	TGTGGTGCCCGCTATGATACTT
869	22	60	50	TGTGGTGCCCGCTATGATACTT
869	22	60	50	TGTGGTGCCCGCTATGATACTT
869	22	60	50	TGTGGTGCCCGCTATGATACTT
869	22	60	50	TGTGGTGCCCGCTATGATACTT
869	20	58	55	TGTGGTGCCCGCTATGATAC
869	20	58	55	TGTGGTGCCCGCTATGATAC
869	20	58	55	TGTGGTGCCCGCTATGATAC
869	20	58	55	TGTGGTGCCCGCTATGATAC
869	20	58	55	TGTGGTGCCCGCTATGATAC
868	21	59	57	CTGTGGTGCCCGCTATGATAC
868	21	59	57	CTGTGGTGCCCGCTATGATAC
868	21	59	57	CTGTGGTGCCCGCTATGATAC
868	21	59	57	CTGTGGTGCCCGCTATGATAC
868	21	59	57	CTGTGGTGCCCGCTATGATAC
868	20	58	55	CTGTGGTGCCCGCTATGATA
868	20	58	55	CTGTGGTGCCCGCTATGATA
868	20	58	55	CTGTGGTGCCCGCTATGATA
868	20	58	55	CTGTGGTGCCCGCTATGATA
868	20	58	55	CTGTGGTGCCCGCTATGATA
867	21	60	52	TCTGTGGTGCCCGCTATGATA
867	21	60	52	TCTGTGGTGCCCGCTATGATA
867	21	60	52	TCTGTGGTGCCCGCTATGATA
867	21	60	52	TCTGTGGTGCCCGCTATGATA
867	21	60	52	TCTGTGGTGCCCGCTATGATA
867	20	60	55	TCTGTGGTGCCCGCTATGAT
867	20	60	55	TCTGTGGTGCCCGCTATGAT
867	20	60	55	TCTGTGGTGCCCGCTATGAT
867	20	60	55	TCTGTGGTGCCCGCTATGAT
867	20	60	55	TCTGTGGTGCCCGCTATGAT
864	20	60	60	GTGTCTGTGGTGCCCGCTAT
864	20	60	60	GTGTCTGTGGTGCCCGCTAT
864	20	60	60	GTGTCTGTGGTGCCCGCTAT

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FIG. 5B

Forward Primer				
Start	Length	Tm	%GC	Primer
864	20	60	60	GTGTCTGTGGTGCCCGCTAT
864	20	60	60	GTGTCTGTGGTGCCCGCTAT
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	23	68	48	AGACAGTGGCACTGTGACCATAA
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3739	24	69	46	AGACAGTGGCACTGTGACCATAAT
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	23	68	48	AAGACAGTGGCACTGTGACCATA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA

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FIG. 5C

Forward Primer				
Start	Length	Tm	%GC	Primer
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3738	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	23	58	48	AAGACAGTGGCACTGTGACCATA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	24	60	46	AAGACAGTGGCACTGTGACCATAA
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3738	25	60	44	AAGACAGTGGCACTGTGACCATAAT
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA



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FIG. 5D

Forward Primer				
Start	Length	Tm	%GC	Primer
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3737	24	60	50	GAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3736	25	61	48	AGAAGACAGTGGCACTGTGACCATA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	24	59	46	AGACAGTGGCACTGTGACCATAAT
3739	23	58	48	AGACAGTGGCACTGTGACCATAA
3739	23	58	48	AGACAGTGGCACTGTGACCATAA

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FIG. 5E

[illegible]

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FIG. 5F

				Probe
Start	Length	Tm	%GC	Probe
1536	25	70	52	CTGGGCCATTTTGAACCTCGGGAA
1536	23	68	57	CTGGGCCATTTTGAACCTCGGG
1536	24	69	54	CTGGGCCATTTTGAACCTCGGGA
1548	25	70	48	TGAACCTCGGGAATTGCCAAAAGCA
1534	24	68	54	CACTGGGCCATTTTGAACCTCGG
1532	25	70	52	TGCACTGGGCCATTTTGAACCTCG
1535	24	68	54	ACTGGGCCATTTTGAACCTCGGG
1534	25	70	56	CACTGGGCCATTTTGAACCTCGGG
1537	23	69	52	TGGGCCATTTTGAACCTCGGGA
1535	25	70	52	ACTGGGCCATTTTGAACCTCGGGA
1537	25	69	48	TGGGCCATTTTGAACCTCGGGAAT
1537	24	70	50	TGGGCCATTTTGAACCTCGGGAA
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
961	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
963	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
960	25	71	56	TCATGTGCAAGTCGAAAGGGCCTGC
962	24	69	54	ATGTGCAAGTCGAAAGGGCCTGCA
960	24	68	54	TCATGTGCAAGTCGAAAGGGCCTG

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FIG. 5G

Probe				
Start	Length	Tm	%GC	Probe
981	24	69	58	CATGTGCAAGTCGAAAGGGCCTGC
983	23	70	57	TGTGCAAGTCGAAAGGGCCTGCA
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAGGGTCATGOACCGG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG

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FIG. 5H

Probe				
Start	Length	Tm	%GC	Probe
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3849	24	70	58	TAACCGCAGAAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAAGGGTCATGCACCG

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FIG. 5I

Probe				
Start	Length	Tm	%GC	Probe
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3852	21	69	67	CCGCAGAAGGGTCATGCACCGG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCGG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAGGGTCATGCACCGG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3855	23	68	61	CAGAAGGGTCATGCACCGGCTGT
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG

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FIG. 5J

Probe				
Start	Length	Tm...	%GC	Probe
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3855	23	68	61	CAGAAAGGGTCATGCACCGGCTGT
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG
3848	25	69	56	ATAACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3855	23	68	61	CAGAAAGGGTCATGCACCGGCTGT
3849	24	70	58	TAACCGCAGAAGGGTCATGCACCG
3850	23	70	61	AACCGCAGAAGGGTCATGCACCG
3852	21	69	67	CCGCAGAAAGGGTCATGCACCG
3851	22	69	64	ACCGCAGAAGGGTCATGCACCG
3853	21	69	67	CGCAGAAAGGGTCATGCACCGG

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FIG. 5K

Reverse Primer					Amplicon				
Start	Length	Tm	%GC	Primer	Length	Tm	%GC	Ta	Penalty
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1820	25	58	40	AGTCCCTTTAACTGAGTTGCAATGT	151	77	44	57	11.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	43.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	43.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	43.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	43.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	43.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	45.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	45.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	45.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	45.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	158	78	44	57	45.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	49.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	49.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	49.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	49.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	49.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	50.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	50.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	50.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	50.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	159	78	45	57	50.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	54.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	54.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	54.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	54.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	54.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	55.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	55.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	55.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	55.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	160	78	44	57	55.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	163	78	45	57	70.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	163	78	45	57	70.0
1026	25	58	44	AAGGTTAAGACCACTACCGCAGTAA	163	78	45	57	70.0



FIG. 5L

[illegible]

FIG. 5M

[illegible]

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FIG. 5N

Reverse Primer				Amplicon					
Start	Length	Tm	%GC	Primer	Length	Tm	%GC	Ta	Penalty
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	189	75	39	56	197.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	189	75	39	56	197.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	189	75	39	56	197.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3925	22	60	45	TGTGGTGTGCAACGTTAATTCG	190	75	38	56	203.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	211.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	22	59	41	TCAATTGTGGTGTGCAACGTTA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	212.0
3930	23	60	39	TCAATTGTGGTGTGCAACGTTAA	192	75	38	55	213.0
3930	24	60	38	TCAATTGTGGTGTGCAACGTTAAT	192	75	38	55	213.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	213.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	213.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	213.0
3930	21	59	43	TCAATTGTGGTGTGCAACGTT	192	75	38	55	213.0
3930	24	60	38	TCAATTGTGGTGTGCAACGTTAAT	192	75	38	55	213.0
3930	24	60	38	TCAATTGTGGTGTGCAACGTTAAT	192	75	38	55	213.0

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FIG. 50

[illegible]

FIG. 6A

[illegible]

FIG. 6B

[illegible]

FIG. 6C

[illegible]

FIG. 6D

[illegible]



FIG. 6E

[illegible]

FIG. 6F

Probe				
Start	Length	Tm	%GC	Probe
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
584	25	69	52	TCAAGCAAGGCATGATGG ACCCTCA
585	25	69	52	CAAGCAAGGCATGATGG ACCCTCAA
105	25	69	48	TGTCGCATCAACAGGTGCAAATGGA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACA GTGGGCCA
585	25	69	52	CAAGCAAGGCATGATGG ACCCTCAA
584	25	69	52	TCAAGCAAGGCATGATGG ACCCTCA
585	25	69	52	CAAGCAAGGCATGATGG ACCCTCAA
584	25	69	52	TCAAGCAAGGCATGATGG ACCCTCA
105	25	69	48	TGTCGCATCAACAGGTGCAAATGGA
105	25	69	48	TGTCGCATCAACAGGTGCAAATGGA
105	25	69	48	TGTCGCATCAACAGGTGCAAATGGA
215	23	72	61	ATGCCGCAAAGGCCAAG GCTGCT
215	21	69	62	ATGCCGCAAAGGCCAAG GCTG
218	22	69	64	CCGCAAAGGCCAAGGCT GCTCT
218	24	71	63	CCGCAAAGGCCAAGGCT GCTCTCT
213	21	69	62	CAATGCCGCAAAGGCCA AGGC
212	22	71	59	TCAATGCCGCAAAGGCCA AGGC
213	23	72	61	CAATGCCGCAAAGGCCA AGGCTG
224	22	70	68	AGGCCAAGGCTGCTCTCTCGCG
223	24	71	63	AAGGCCAAGGCTGCTCTCTCGCGT
227	24	68	63	CCAAGGCTGCTCTCTCGCGTAAGC
219	23	69	61	CGCAAAGGCCAAGGCTGCTCTCT
221	24	70	63	CAAAGGCCAAGGCTGCTCTCTCGC
224	24	70	63	AGGCCAAGGCTGCTCTCTCGCGTA
222	25	71	60	AAAGGCCAAGGCTGCTCTCTCGCGT
211	23	71	61	CTCAATGCCGCAAAGGCCAAGGC
206	23	69	57	TCTTCCTCAATGCCGCAAAGGCC
207	23	70	57	CTTCCTCAATGCCGCAAAGGCCA
206	24	71	54	TCTTCCTCAATGCCGCAAAGGCCA
205	25	72	52	TTCTTCCTCAATGCCGCAAAGGCCA
203	25	69	52	TCTTCCTCAATGCCGCAAAGGCC
204	25	70	56	CTTCTTCCTCAATGCCGCAAAGGCC
205	24	70	54	TTCTTCCTCAATGCCGCAAAGGCC
209	23	70	57	TCCTCAATGCCGCAAAGGCCAAG
210	23	71	61	CCTCAATGCCGCAAAGGCCAAGG

## FIG. 6G

Probe				
Start	Length	Tm	%GC	Probe
209	21	69	57	TCCTCAATGCCGCAAAGGCCA
208	23	70	52	TTCCTCAATGCCGCAAAGGCCAA
207	25	71	56	CTTCCTCAATGCCGCAAAGGCCAAG
213	22	70	59	CAATGCCGCAAAGGCCAAGGCT
218	21	69	67	CCGCAAAGGCCAAGGCTGCTC
212	23	71	57	TCAATGCCGCAAAGGCCAAGGCT
206	25	72	52	TCTTCCTCAATGCCGCAAAGGCCAA
215	22	72	64	ATGCCGCAAAGGCCAAGGCTGC
214	22	70	59	AATGCCGCAAAGGCCAAGGCTG
216	20	69	65	TGCCGCAAAGGCCAAGGCTG
211	24	71	58	CTCAATGCCGCAAAGGCCAAGGCT
208	24	70	54	TTCCTCAATGCCGCAAAGGCCAAG
208	22	69	55	TTCCTCAATGCCGCAAAGGCCA
207	24	70	54	CTTCCTCAATGCCGCAAAGGCCAA
209	22	69	55	TCCTCAATGCCGCAAAGGCCAA
210	22	68	59	CCTCAATGCCGCAAAGGCCAAG
211	22	68	59	CTCAATGCCGCAAAGGCCAAGG
224	23	70	65	AGGCCAAGGCTGCTCTCTCGCGT
216	21	72	67	TGCCGCAAAGGCCAAGGCTGC
227	25	70	64	CCAAGGCTGCTCTCTCGCGTAAGCC
228	25	70	60	CAAGGCTGCTCTCTCGCGTAAGCCA
229	24	68	58	AAGGCTGCTCTCTCTCGCGTAAGCCA
224	25	70	60	AGGCCAAGGCTGCTCTCTCGCGTAA
229	25	68	60	AAGGCTGCTCTCTCTCGCGTAAGCCAG
223	25	70	60	AAGGCCAAGGCTGCTCTCTCGCGTA
218	23	71	65	CCGCAAAGGCCAAGGCTGCTCTC
219	24	70	63	CGCAAAGGCCAAGGCTGCTCTCTC
219	22	68	64	CGCAAAGGCCAAGGCTGCTCTC
223	23	70	65	AAGGCCAAGGCTGCTCTCTCGCG
228	24	68	63	CAAGGCTGCTCTCTCGCGTAAGCC
222	24	71	63	AAAGGCCAAGGCTGCTCTCTCGCG
219	22	68	64	CGCAAAGGCCAAGGCTGCTCTC
216	20	69	65	TGCCGCAAAGGCCAAGGCTG
218	21	69	67	CCGCAAAGGCCAAGGCTGCTC
215	22	72	64	ATGCCGCAAAGGCCAAGGCTGC
218	23	71	65	CCGCAAAGGCCAAGGCTGCTCTC
214	22	70	59	AATGCCGCAAAGGCCAAGGCTG
213	22	70	59	CAATGCCGCAAAGGCCAAGGCT
223	25	70	60	AAGGCCAAGGCTGCTCTCTCGCGTA
224	23	70	65	AGGCCAAGGCTGCTCTCTCGCGT
224	25	70	60	AGGCCAAGGCTGCTCTCTCGCGTAA
219	24	70	63	CGCAAAGGCCAAGGCTGCTCTCTC
222	24	71	63	AAAGGCCAAGGCTGCTCTCTCGCG
223	23	70	65	AAGGCCAAGGCTGCTCTCTCGCG
206	25	72	52	TCTTCCTCAATGCCGCAAAGGCCAA

FIG. 6H

Probe				
Start	Length	Tm	%GC	Probe
210	22	68	59	CCTCAATGCCGCAAAGGCCAAG
205	25	72	52	TTCTTCCTCAATGCCGCAAAGGCCA
204	25	70	56	CTTCTTCCTCAATGCCGCAAAGGCC
206	23	69	57	TCTTCCTCAATGCCGCAAAGGCC
206	24	71	54	TCTTCCTCAATGCCGCAAAGGCCA
205	24	70	54	TTCTTCCTCAATGCCGCAAAGGCC
211	24	71	58	CTCAATGCCGCAAAGGCCAAGGCT
209	22	69	55	TCCTCAATGCCGCAAAGGCCAA
207	24	70	54	CTTCCTCAATGCCGCAAAGGCCAA
203	25	69	52	TCTTCCTTCCTCAATGCCGCAAAGGC
208	24	70	54	TTCTTCCTCAATGCCGCAAAGGCCAAG
211	22	68	59	CTCAATGCCGCAAAGGCCAAGG
208	22	69	55	TTCTTCCTCAATGCCGCAAAGGCCA
213	21	69	62	CAATGCCGCAAAGGCCAAGGC
213	23	72	61	CAATGCCGCAAAGGCCAAGGCTG
211	23	71	61	CTCAATGCCGCAAAGGCCAAGGC
212	22	71	59	TCAATGCCGCAAAGGCCAAGGC
212	23	71	57	TCAATGCCGCAAAGGCCAAGGCT
216	21	72	67	TGCCGCAAAGGCCAAGGCTGC
216	23	72	61	ATGCCGCAAAGGCCAAGGCTGCT
216	21	69	62	ATGCCGCAAAGGCCAAGGCTG
208	23	70	52	TTCTTCCTCAATGCCGCAAAGGCCAA
207	25	71	56	CTTCCTCAATGCCGCAAAGGCCAAG
210	23	71	61	CCTCAATGCCGCAAAGGCCAAGG
209	21	69	57	TCCTCAATGCCGCAAAGGCCA
207	23	70	57	CTTCCTCAATGCCGCAAAGGCCA
209	23	70	57	TCCTCAATGCCGCAAAGGCCAAG
228	24	68	63	CAAGGCTGCTCTCTCGCGTAAGCC
227	25	70	64	CCAAGGCTGCTCTCTCGCGTAAGCC
227	24	68	63	CCAAGGCTGCTCTCTCGCGTAAGC
224	24	70	63	AGGCCAAGGCTGCTCTCTCGCGTA
229	24	68	58	AAGGCTGCTCTCTCGCGTAAGCCA
218	22	69	64	CCGCAAAGGCCAAGGCTGCTCT
229	25	68	60	AAGGCTGCTCTCTCGCGTAAGCCAG
228	25	70	60	CAAGGCTGCTCTCTCGCGTAAGCCA
218	24	71	63	CCGCAAAGGCCAAGGCTGCTCTCT
221	24	70	63	CAAAGGCCAAGGCTGCTCTCTCGC
219	23	69	61	CGCAAAGGCCAAGGCTGCTCTCT
224	22	70	68	AGGCCAAGGCTGCTCTCTCGCG
223	24	71	63	AAGGCCAAGGCTGCTCTCTCGCGT
222	25	71	60	AAAGGCCAAGGCTGCTCTCTCGCGT
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA

FIG. 6I

Probe				
Start	Length	Tm	%GC	Probe
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
474	25	71	60	TGGTGTAGGATGGGACAGTGGGCCA
584	25	69	52	TCAAGCAAGGCATGATGGACCCTCA
585	25	69	52	CAAGCAAGGCATGATGGACCCTCAA
584	25	69	52	TCAAGCAAGGCATGATGGACCCTCA
585	25	69	52	CAAGCAAGGCATGATGGACCCTCAA
584	25	69	52	TCAAGCAAGGCATGATGGACCCTCA
585	25	69	52	CAAGCAAGGCATGATGGACCCTCAA
222	25	71	60	AAAGGCCAAGGCTGCTCTCTCGCGT
218	24	71	63	CCGCAAAGGCCAAGGCTGCTCTCT
218	23	71	65	CCGCAAAGGCCAAGGCTGCTCTC
224	25	70	60	AGGCCAAGGCTGCTCTCTCGCGTAA
224	22	70	68	AGGCCAAGGCTGCTCTCTCGCG
224	23	70	65	AGGCCAAGGCTGCTCTCTCGCGT
224	24	70	63	AGGCCAAGGCTGCTCTCTCGCGTA
216	20	69	65	TGCCGCAAAGGCCAAGGCTG
215	23	72	61	ATGCCGCAAAGGCCAAGGCTGCT
218	21	69	67	CCGCAAAGGCCAAGGCTGCTC
216	21	72	67	TGCCGCAAAGGCCAAGGCTGC
219	22	68	64	CGCAAAGGCCAAGGCTGCTCTC
219	23	69	61	CGCAAAGGCCAAGGCTGCTCTCT
229	25	68	60	AAGGCTGCTCTCTCGCGTAAGCCAG
228	25	70	60	CAAGGCTGCTCTCTCGCGTAAGCCA
227	24	68	63	CCAAGGCTGCTCTCTCGCGTAAGC
229	24	68	58	AAGGCTGCTCTCTCGCGTAAGCCA
228	24	68	63	CAAGGCTGCTCTCTCGCGTAAGCC
223	25	70	60	AAGGCCAAGGCTGCTCTCTCGCGTA
227	25	70	64	CCAAGGCTGCTCTCTCGCGTAAGCC
223	24	71	63	AAGGCCAAGGCTGCTCTCTCGCGT
223	23	70	65	AAGGCCAAGGCTGCTCTCTCGCG
218	22	69	64	CCGCAAAGGCCAAGGCTGCTCT
221	24	70	63	CAAAGGCCAAGGCTGCTCTCTCGC
219	24	70	63	CGCAAAGGCCAAGGCTGCTCTCTC
222	24	71	63	AAAGGCCAAGGCTGCTCTCTCGCG
207	25	71	56	CTTCCTCAATGCCGCAAAGGCCAAG
208	24	70	54	TTCCTCAATGCCGCAAAGGCCAAG
208	23	70	52	TTCCTCAATGCCGCAAAGGCCAA
211	22	68	59	CTCAATGCCGCAAAGGCCAAGG
206	25	72	52	TCTTCCTCAATGCCGCAAAGGCCAA
207	23	70	57	CTTCCTCAATGCCGCAAAGGCCA
207	24	70	54	CTTCCTCAATGCCGCAAAGGCCAA
203	25	69	52	TCTTCCTTCCTCAATGCCGCAAAGGC

FIG. 6J

Probe				
Start	Length	Tm	%GC	Probe
206	24	71	54	TCTTCCTCAATGCCGCAAAGGCCA
205	24	70	54	TTCTTCCTCAATGCCGCAAAGGCC
204	25	70	56	CTTCTTCCTCAATGCCGCAAAGGCC
208	22	69	55	TTCCTCAATGCCGCAAAGGCCA
206	23	69	57	TCTTCCTCAATGCCGCAAAGGCC
205	25	72	52	TTCTTCCTCAATGCCGCAAAGGCCA
214	22	70	59	AATGCCGCAAAGGCCAAGGCTG
209	23	70	57	TCCTCAATGCCGCAAAGGCCAAG
210	23	71	61	CCTCAATGCCGCAAAGGCCAAGG
211	23	71	61	CTCAATGCCGCAAAGGCCAAGGC
209	22	69	55	TCCTCAATGCCGCAAAGGCCAA
209	21	69	57	TCCTCAATGCCGCAAAGGCCA
213	21	69	62	CAATGCCGCAAAGGCCAAGGC
213	23	72	61	CAATGCCGCAAAGGCCAAGGCTG
211	24	71	58	CTCAATGCCGCAAAGGCCAAGGCT
215	21	69	62	ATGCCGCAAAGGCCAAGGCTG
210	22	68	59	CCTCAATGCCGCAAAGGCCAAG
212	23	71	57	TCAATGCCGCAAAGGCCAAGGCT
213	22	70	59	CAATGCCGCAAAGGCCAAGGCT
212	22	71	59	TCAATGCCGCAAAGGCCAAGGC

FIG. 6K

[illegible]

FIG. 6L

[illegible]



FIG. 6M

[illegible]



FIG. 60

[illegible]

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FIG. 7A

Forward Primer				
Start	Length	Tm	%GC	Primer
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6062	21	59	43	AAAGTCGGGCTTGACGAATTT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6061	22	59	41	TAAAGTCGGGCTTGACGAATTT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6060	22	59	41	TTAAAGTCGGGCTTGACGAATT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6060	23	60	39	TTAAAGTCGGGCTTGACGAATTT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6058	25	62	40	GATTAAAGTCGGGCTTGACGAATTT
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA

FIG. 7B

Forward Primer				
Start	Length	Tm	%GC	Primer
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6059	23	59	39	ATTAAAGTCGGGCTTGACGAATT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6058	25	62	40	GATTAAAGTCGGGCTTGACGAATTT
6059	24	60	38	ATTAAAGTCGGGCTTGACGAATTT
6058	25	62	40	GATTAAAGTCGGGCTTGACGAATTT
6058	22	59	45	GATTAAAGTCGGGCTTGACGAA
6058	23	59	43	GATTAAAGTCGGGCTTGACGAAT
6058	24	61	42	GATTAAAGTCGGGCTTGACGAATT
6058	25	62	40	GATTAAAGTCGGGCTTGACGAATTT
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6054	22	59	45	CAAGGATTAAAGTCGGGCTTGA
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6054	23	60	48	CAAGGATTAAAGTCGGGCTTGAC
6052	24	62	42	TTCAAGGATTAAAGTCGGGCTTGA
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6052	24	62	42	TTCAAGGATTAAAGTCGGGCTTGA
6053	23	61	43	TCAAGGATTAAAGTCGGGCTTGA
6052	24	62	42	TTCAAGGATTAAAGTCGGGCTTGA
6053	24	61	46	TCAAGGATTAAAGTCGGGCTTGAC
6052	24	62	42	TTCAAGGATTAAAGTCGGGCTTGA

FIG. 7C

[illegible]

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FIG. 7D

[illegible]

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FIG. 7E

Reverse Primer					Amplicon				
Start	Length	Tm	%GC	Primer	Length	Tm	%GC	Ta	Penalty
6298	23	59	48	CGGACAGAAACTCTAAGCCATCA	235	74	35	54	427.0
6298	24	59	46	CGGACAGAAACTCTAAGCCATCAT	235	74	35	54	428.0
6298	25	61	44	CGGACAGAAACTCTAAGCCATCATT	235	74	35	54	429.0
6298	23	59	48	CGGACAGAAACTCTAAGCCATCA	236	74	35	54	431.0
6298	24	59	46	CGGACAGAAACTCTAAGCCATCAT	236	74	35	54	432.0
6298	25	61	44	CGGACAGAAACTCTAAGCCATCATT	236	74	35	54	433.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	236	74	35	54	433.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	236	74	35	54	434.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	237	74	35	54	436.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	237	74	35	54	437.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	237	74	35	54	437.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	237	74	35	54	437.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	237	74	35	54	438.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	237	74	35	54	438.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	237	74	35	54	438.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	237	74	35	55	439.0
6298	25	61	44	ATCGGACAGAAACTCTAAGCCATCA	237	74	35	54	439.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	238	74	35	54	442.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	238	74	35	54	442.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	238	74	35	54	443.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	238	74	35	54	443.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	238	74	35	55	443.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	238	74	35	54	443.0
6298	25	61	44	ATCGGACAGAAACTCTAAGCCATCA	238	74	35	54	443.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	238	74	35	54	444.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	238	74	35	54	444.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	238	74	35	55	444.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	238	74	35	55	445.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	239	74	35	54	446.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	239	74	35	54	447.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	239	74	35	54	447.0
6296	23	59	48	CGGACAGAAACTCTAAGCCATCA	239	74	35	54	448.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	239	74	35	54	448.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	239	74	35	55	448.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	239	74	35	54	448.0
6298	25	61	44	ATCGGACAGAAACTCTAAGCCATCA	239	74	35	54	448.0
6296	24	59	46	CGGACAGAAACTCTAAGCCATCAT	239	74	35	55	449.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	239	74	35	55	449.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	239	74	35	55	449.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	239	74	35	54	449.0
6298	25	61	44	ATCGGACAGAAACTCTAAGCCATCA	239	74	35	55	449.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	239	74	35	55	450.0
6297	25	61	44	TCGGACAGAAACTCTAAGCCATCAT	239	74	35	55	450.0
6296	25	61	44	CGGACAGAAACTCTAAGCCATCATT	239	74	35	55	451.0
6297	24	61	46	TCGGACAGAAACTCTAAGCCATCA	240	74	35	54	452.0



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FIG. 7F

Reverse Primer					Amplicon				
Start	Length	Tm	%GC	Primer	Length	Tm	%GC	Ta	Penalty
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	240	74	35	54	453.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	240	74	35	54	453.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	240	74	35	54	454.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	240	74	35	55	454.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	240	73	35	54	454.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	240	74	35	55	455.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	240	74	35	55	455.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	240	73	35	55	455.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	240	74	35	55	456.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	241	74	35	54	458.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	241	74	35	54	459.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	241	74	35	55	460.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	241	74	35	55	461.0
6296	23	59	48	CGGACAGAAACTCTAACCCATCA	243	74	35	54	466.0
6296	24	59	46	CGGACAGAAACTCTAACCCATCAT	243	74	35	55	467.0
6296	23	59	48	CGGACAGAAACTCTAACCCATCA	243	74	35	54	467.0
6296	25	61	44	CGGACAGAAACTCTAACCCATCATT	243	74	35	55	468.0
6296	24	59	46	CGGACAGAAACTCTAACCCATCAT	243	74	35	55	468.0
6296	25	61	44	CGGACAGAAACTCTAACCCATCATT	243	74	35	55	469.0
6296	23	59	48	CGGACAGAAACTCTAACCCATCA	244	74	35	54	472.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	244	74	35	54	472.0
6296	24	59	46	CGGACAGAAACTCTAACCCATCAT	244	74	35	55	473.0
6296	23	59	48	CGGACAGAAACTCTAACCCATCA	244	74	35	54	473.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	244	74	35	55	473.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	244	74	35	54	473.0
6296	25	61	44	CGGACAGAAACTCTAACCCATCATT	244	74	35	55	474.0
6296	24	59	46	CGGACAGAAACTCTAACCCATCAT	244	74	35	55	474.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	244	74	35	55	474.0
6296	25	61	44	CGGACAGAAACTCTAACCCATCATT	244	74	35	55	475.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	245	74	35	55	478.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	245	74	35	54	478.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	245	74	35	55	479.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	245	74	35	55	479.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	245	74	35	55	479.0
6296	25	61	44	CGGACAGAAACTCTAACCCATCATT	245	74	35	55	480.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	245	74	35	55	480.0
6297	24	61	46	TCGGACAGAAACTCTAACCCATCA	246	74	35	55	484.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	246	74	35	55	484.0
6297	25	61	44	TCGGACAGAAACTCTAACCCATCAT	246	74	35	55	485.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	246	74	35	55	485.0
6298	25	61	44	ATCGGACAGAAACTCTAACCCATCA	247	74	35	55	490.0

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## Envelope Protein Purification Flow-Chart

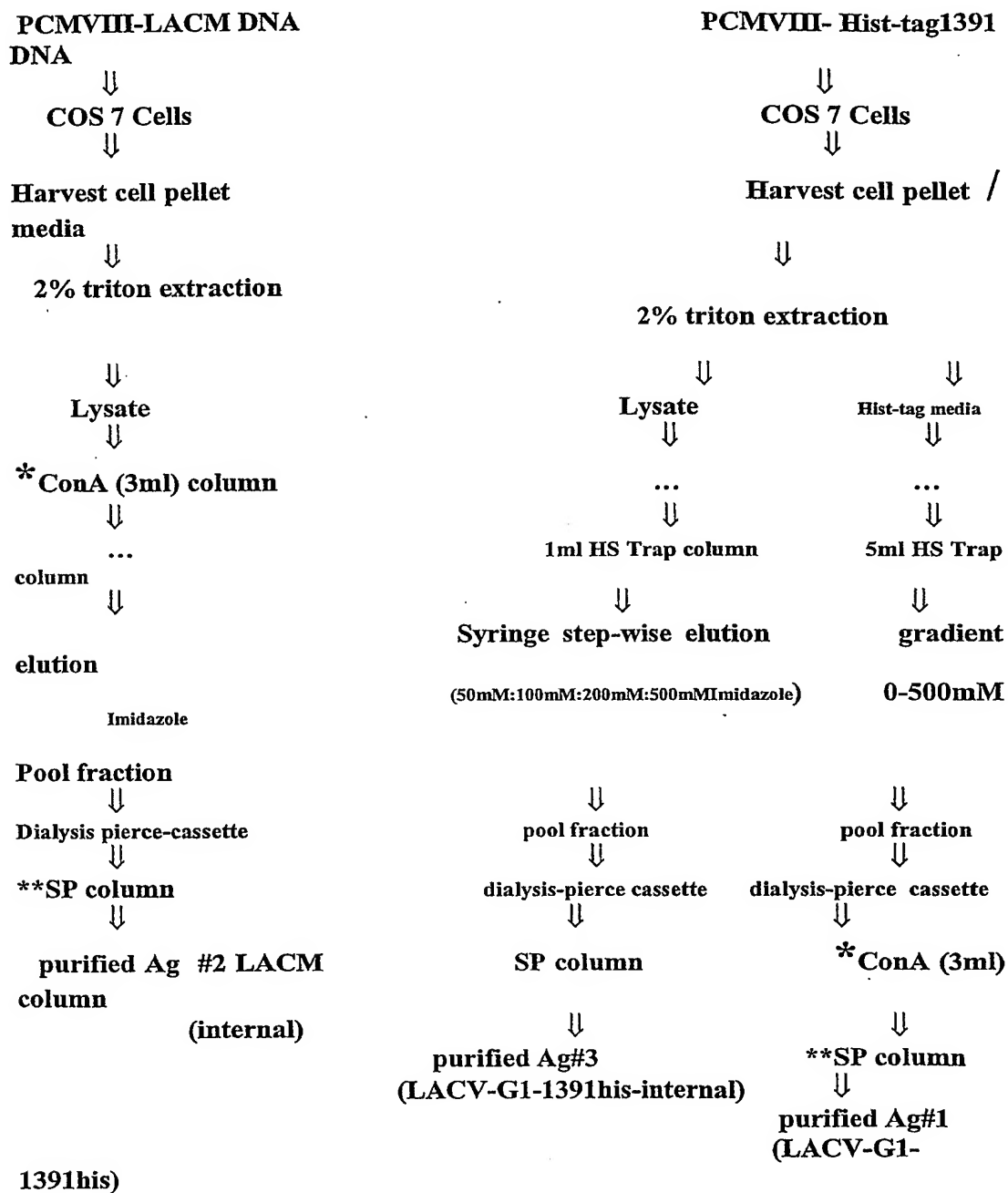


FIGURE 8

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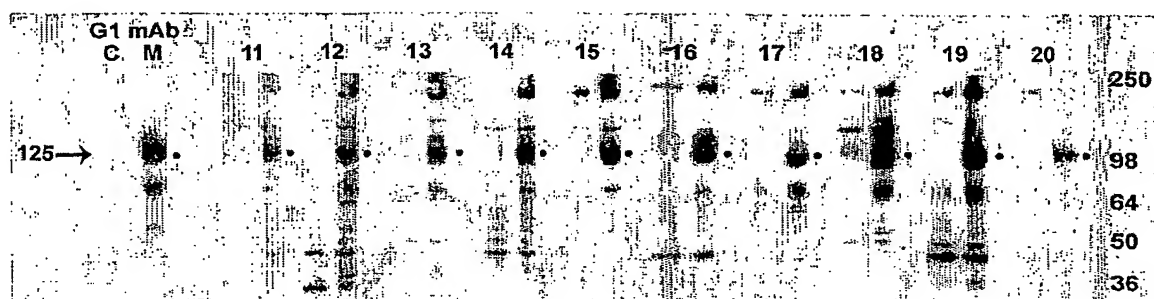


Figure 9A

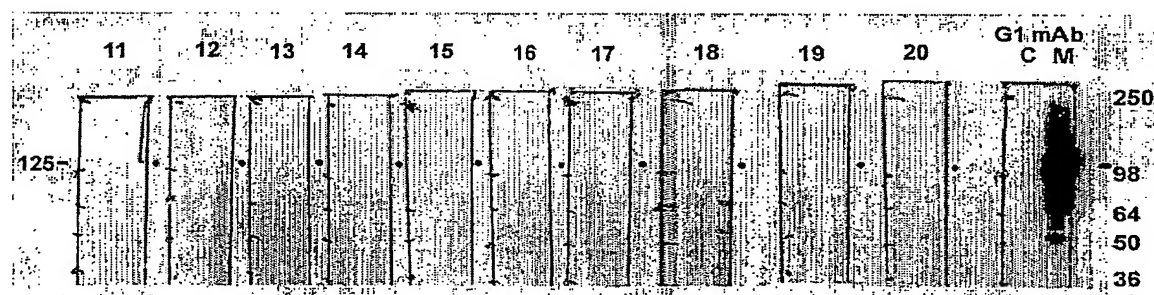
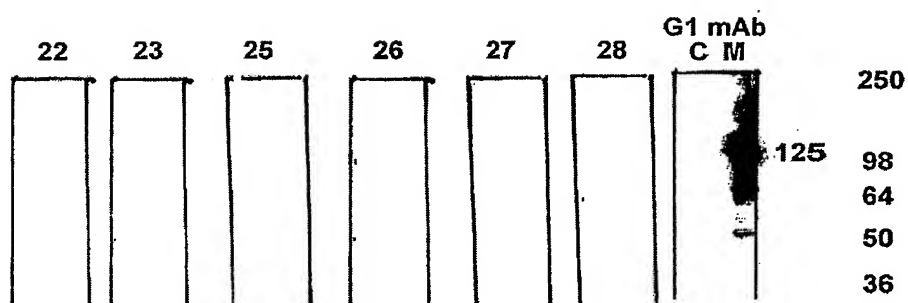


Figure 9B

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**Figure 10A****Figure 10B**

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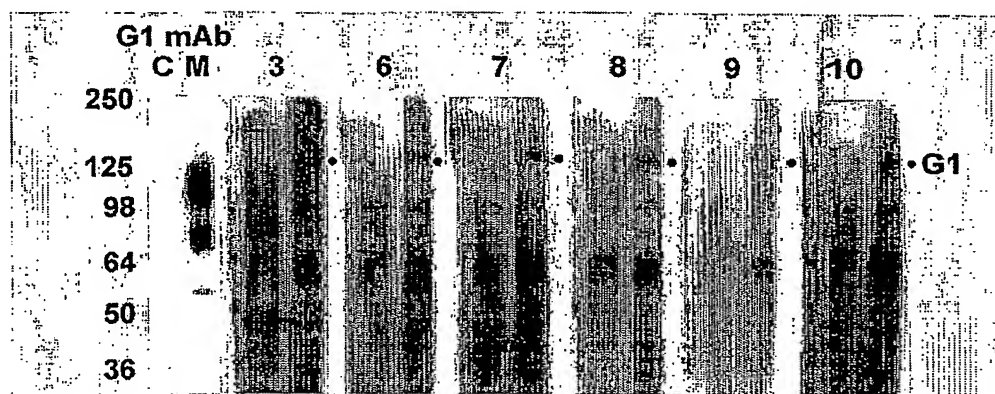


Figure 11A

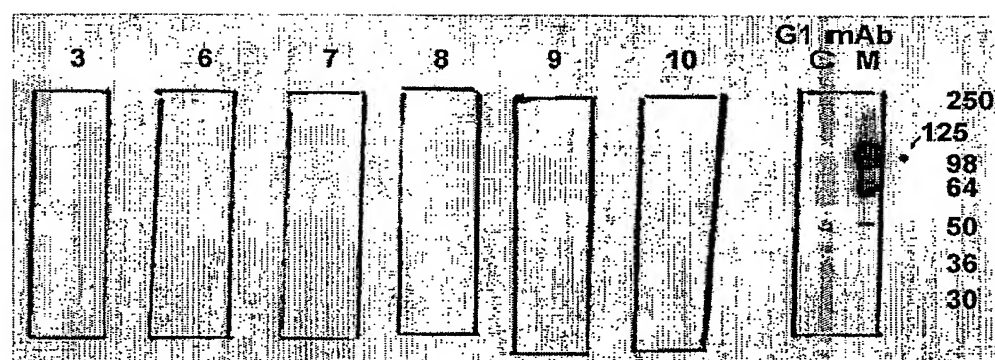


Figure 11B

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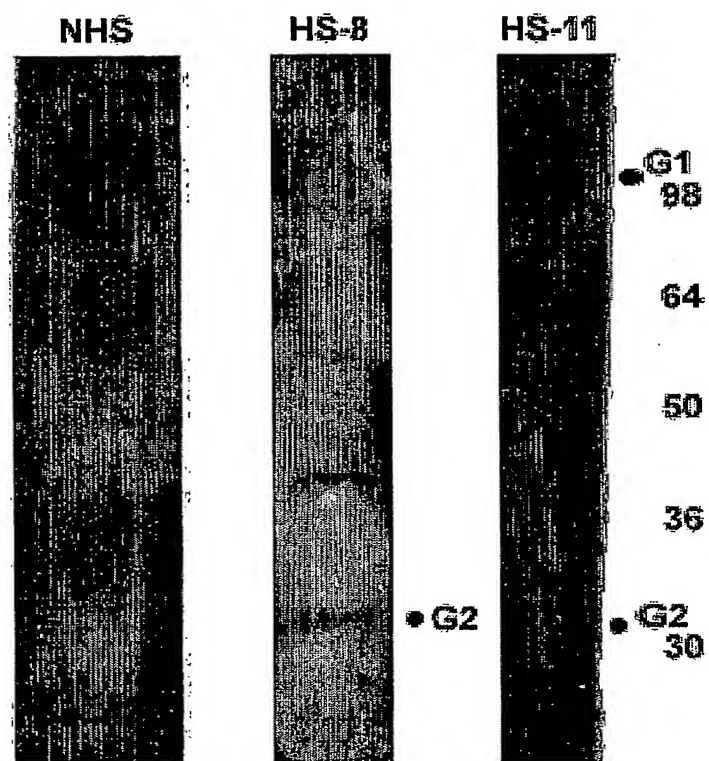


FIGURE 12A

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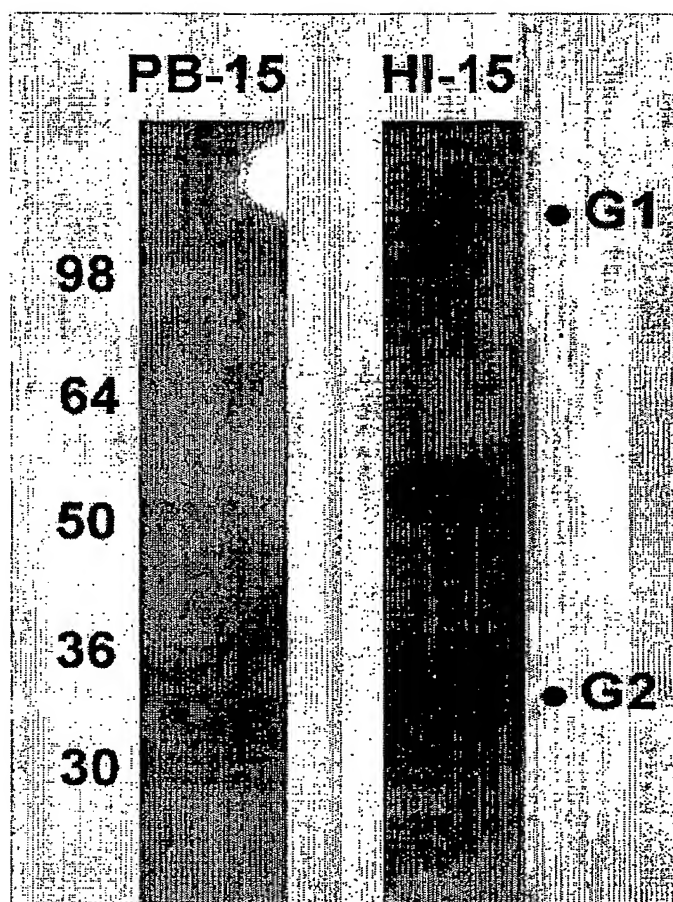


FIGURE 12B